

SEQUENCE LISTING

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<120> PREFERRED SEGMENTS OF NEURAL THREAD PROTEIN AND METHODS
OF USING THE SAME

<130> 18792-177

<140> 09/697,590

<141> 2000-10-27

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 1442

<212> DNA

<213> Unknown Organism

<220>

<221> CDS

<222> (15)..(1139)

<220>

<223> Description of Unknown Organism: NTP DNA sequence

<400> 1

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Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys
1 5 10

aat ggc gca atc tca gct cac cgc aac ctc cgc ctc ccg ggt tca agc 98
Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser
15 20 25

gat tct cct gcc tca gcc tcc cca gta gct ggg att aca ggc atg tgc 146
Asp Ser Pro Ala Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys
30 35 40

acc cac gct cgg cta att ttg tat ttt ttt tta gta gag atg gag ttt 194
Thr His Ala Arg Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe
45 50 55 60

ctc cat gtt ggt cag gct ggt ctc gaa ctc ccg acc tca gat gat ccc 242
Leu His Val Gly Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro
65 70 75

tcc gtc tcg gcc tcc caa agt gct aga tac agg act ggc cac cat gcc 290
Ser Val Ser Ala Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala
80 85 90



a6

cg	ctc	tgc	ctg	gct	aat	ttt	tgt	ggt	aga	aac	agg	gtt	tca	ctg	atg	338
Arg	Leu	Cys	Leu	Ala	Asn	Phe	Cys	Gly	Arg	Asn	Arg	Val	Ser	Leu	Met	
		95					100					105				
tgc	cca	agc	tgg	tct	cct	gag	ctc	aag	cag	tcc	acc	tgc	ctc	agc	ctc	386
Cys	Pro	Ser	Trp	Ser	Pro	Glu	Leu	Lys	Gln	Ser	Thr	Cys	Leu	Ser	Leu	
	110					115					120					
cca	aag	tgc	tgg	gat	tac	agg	cgt	gca	gcc	gtg	cct	ggc	ctt	ttt	att	434
Pro	Lys	Cys	Trp	Asp	Tyr	Arg	Arg	Ala	Ala	Val	Pro	Gly	Leu	Phe	Ile	
125					130					135					140	
tta	ttt	ttt	tta	aga	cac	agg	tgt	ccc	act	ctt	acc	cag	gat	gaa	gtg	482
Leu	Phe	Phe	Leu	Arg	His	Arg	Cys	Pro	Thr	Leu	Thr	Gln	Asp	Glu	Val	
				145					150					155		
cag	tgg	tgt	gat	cac	agc	tca	ctg	cag	cct	tca	act	cct	gag	atc	aag	530
Gln	Trp	Cys	Asp	His	Ser	Ser	Leu	Gln	Pro	Ser	Thr	Pro	Glu	Ile	Lys	
			160					165					170			
cat	cct	cct	gcc	tca	gcc	tcc	caa	gta	gct	ggg	acc	aaa	gac	atg	cac	578
His	Pro	Pro	Ala	Ser	Ala	Ser	Gln	Val	Ala	Gly	Thr	Lys	Asp	Met	His	
	175						180					185				
cac	tac	acc	tgg	cta	att	ttt	att	ttt	att	ttt	aat	ttt	ttg	aga	cag	626
His	Tyr	Thr	Trp	Leu	Ile	Phe	Ile	Phe	Ile	Phe	Asn	Phe	Leu	Arg	Gln	
	190					195					200					
agt	ctc	aac	tct	gtc	acc	cag	gct	gga	gtg	cag	tgg	cgc	aat	ctt	ggc	674
Ser	Leu	Asn	Ser	Val	Thr	Gln	Ala	Gly	Val	Gln	Trp	Arg	Asn	Leu	Gly	
205					210					215					220	
tca	ctg	caa	cct	ctg	cct	ccc	ggg	ttc	aag	tta	ttc	tcc	tgc	ccc	agc	722
Ser	Leu	Gln	Pro	Leu	Pro	Pro	Gly	Phe	Lys	Leu	Phe	Ser	Cys	Pro	Ser	
			225						230					235		
ctc	ctg	agt	agc	tgg	gac	tac	agg	cgc	cca	cca	cgc	cta	gct	aat	ttt	770
Leu	Leu	Ser	Ser	Trp	Asp	Tyr	Arg	Arg	Pro	Pro	Arg	Leu	Ala	Asn	Phe	
			240					245					250			
ttt	gta	ttt	tta	gta	gag	atg	ggg	ttc	acc	atg	ttc	gcc	agg	ttg	atc	818
Phe	Val	Phe	Leu	Val	Glu	Met	Gly	Phe	Thr	Met	Phe	Ala	Arg	Leu	Ile	
		255					260					265				
ttg	atc	tct	gga	cct	tgt	gat	ctg	cct	gcc	tgc	gcc	tcc	caa	agt	gct	866
Leu	Ile	Ser	Gly	Pro	Cys	Asp	Leu	Pro	Ala	Ser	Ala	Ser	Gln	Ser	Ala	
	270					275					280					
ggg	att	aca	ggc	gtg	agc	cac	cac	gcc	cgg	ctt	att	ttt	aat	ttt	tgt	914
Gly	Ile	Thr	Gly	Val	Ser	His	His	Ala	Arg	Leu	Ile	Phe	Asn	Phe	Cys	
285					290					295					300	
ttg	ttt	gaa	atg	gaa	tct	cac	tct	gtt	acc	cag	gct	gga	gtg	caa	tgg	962
Leu	Phe	Glu	Met	Glu	Ser	His	Ser	Val	Thr	Gln	Ala	Gly	Val	Gln	Trp	
				305					310					315		

ab
Cont

cca aat ctc ggc tca ctg caa cct ctg cct ccc ggg ctc aag cga ttc 1010
 Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe
 320 325 330

tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cac ctg cca cca 1058
 Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro
 335 340 345

cac ccc gct aat ttt tgt att ttc att aga ggc ggg gtt tca cca tat 1106
 His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr
 350 355 360

ttg tca ggc tgg tct caa act cct gac ctc agg tgaccacacct gcctcagcct 1159
 Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg
 365 370 375

tccaaagtgc tgggattaca ggcgtgagcc acctcaccca gccggctaatt ttagataaaaa 1219

aaatatgtag caatggggggg tcttgctatg ttgccaggc tgggtctcaaa cttctggcctt 1279

catgcaatcc ttccaaatga gccacaacac ccagccagtc acatttttta aacagttaca 1339

tctttattttt agtatactag aaagtaatac aataaacatg tcaaacctgc aaattcagta 1399

gtaacagagt tcttttataa cttttaaaca aagctttaga gca 1442

<210> 2

<211> 375

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: NTP amino acid
 sequence

<400> 2

Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys Asn Gly Ala Ile
 1 5 10 15

Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala
 20 25 30

Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg
 35 40 45

Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly
 50 55 60

Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala
 65 70 75 80

Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu
 85 90 95

Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp
 100 105 110

ab
 cont

Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp
 115 120 125
 Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu
 130 135 140
 Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp
 145 150 155 160
 His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala
 165 170 175
 Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp
 180 185 190
 Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser
 195 200 205
 Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro
 210 215 220
 Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser
 225 230 235 240
 Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu
 245 250 255
 Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly
 260 265 270
 Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly
 275 280 285
 Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met
 290 295 300
 Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly
 305 310 315 320
 Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser
 325 330 335
 Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn
 340 345 350
 Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp
 355 360 365
 Ser Gln Thr Pro Asp Leu Arg
 370 375

<210> 3

<211> 6

<212> PRT

<213> Artificial Sequence

 ab
 cont

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 3

His Ala Arg Leu Met Leu
1 5

<210> 4

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic NTP-1 peptide

<400> 4

Leu His Ala Arg Leu Cys Leu Ala Asn Phe Cys Gly Arg Asn Arg Val
1 5 10 15

<210> 5

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic NTP-2 peptide

<400> 5

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<210> 6

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic NTP-3 peptide

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Cys Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Met
1 5 10

<210> 7

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic NTP-4

ab
cont

peptide

<400> 7

His His Ala Arg Leu Pro Leu Ala Asn Phe Cys Gly
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<210> 8

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic NTP-5
 peptide

<400> 8

Arg Thr Gly His His Ala Arg Leu Cys Leu Ala Asn Phe Cys
 1 5 10

<210> 9

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic NTP-6
 peptide

<400> 9

Cys Glu Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys
 1 5 10 15

<210> 10

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic NTP-7
 peptide

<400> 10

Asp Asn Thr His His Ala Arg Leu Ile Leu
 1 5 10

<210> 11

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic NTP-8
 peptide

ab
 Cont

<400> 11
Ser His His Ala Arg Leu Ile Leu
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<210> 12
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 12
Ala Arg Cys Leu
1

ab
ant